Table 1

		SNPs and Deletion Variants			
		7	4	2	9
T	7	,	Primers	Location and Change	Position and Reference Sequence
SEQ ID NO.	Polymorphism ID No.	Sequence	THE		
					0001
	Eloner!	AGGAGCCCCAAAACCTTCTC	5' upstream reg. elem.	5' upstream reg. elem. G/A	GI:18/166 residue 1000
4		TTTTGTG	5' upstream reg. elem.	5' upstream reg. elem. Deletion	GI:187166 residue 472-477
S	Slouia	TO A O A O A O A O A O A O A O A O A O A	5' upstream reg. elem.	5' upstream reg. elem. G/A	GI:187166 residue 559
9	51004a	TCATGIALCGALIAGAGG			
~	SUND WINDS				
	KING WIN DINE		. 4	Location and Change	Position and Reference Sequence
GEO ID NO.	Polymorphism ID No. Sequence	Sequence	Frimers	Location and course.	
200	¥	A Tribling A T \ TO TO THE	5' upstream reg. elem.	5' upstream reg. elem. G/A	GI:187166 residue 84
7	Slonrra	ACHACIMINGCACOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOC	mole was	S' instream reg. elem. G/A	GI:187166 residue 137
80	Slonrrb	TTACAGATCAgTGGACTAGAA	5' upstream reg. elenii.	upancamings cram	

TABLE 2.

SEQ ID NO:	Residue/ Reference Sequence	Probe Sequence
64	1000/GI 187166	AGGAGCGCGCRAAACCTTCTC
65	472-477/GI 187166	TGGACTTAAA (GTTAAA del) TACTTTTG
66	559/GT 187166	TCATGTATCC R ATTAGAGACT

Table 3.

1 S 1 2 1 3 1 3 1 1 3 1 1 1 1 1 1 1 1 1 1 1	NO:	Sequence (5' -> 3') GGGCCAGGGACCAGTGGT	Product Length	ID No.
1 2 1 3)	GGGCCAGGGACCAGTGGT	296	
1 2 1 3		00000100010000		
2 1	LU	AACCGGGTCCCGGACGCA		
3	1	AGGCTCAGGAGACCACGCA	356	
3 3	11	TCCCGCCCTGCACAG		
' <u></u>	12	CATTGGGCATTGTTATTGTTCTTC	313	
	13	AGTTGTAGGTAAGGTGAAGTTTGGG		
	14	TCGTCTGACAGTGTGGGCG	294	
*	15	CCATGAGGAAAGGAGTGAGGGT		
	16		244	
·	1 7	TGGTGTGAAGGGGCTCTGC		
	18	AAGTATCAGACAGGAGAGCAGCATC	213	
6	19	GCCTCGCTTTTCTCCTGGTAG		
	20	CCACTTCCCCAGCCCATCA	228	
7	21	GATTTTTGGTCCGTCTGCTGAG	220	
	22	GAAAGGTGTGCCCCCAG	246	
8	23	TTTCCTTTCCCCCAATGTATCA	246	
	24	GGGCGGTAGCTGGCTGTA		
9	25	GAGCTGCGGGTCCCTGAG	226	
	26	AGATAGGGAGTGAAGGCGGC		
10	27	AGCCACCCGCTCAGGGCA	266	
	28	AGGCAGGGTCCCGGCT		
11	29	TCCGCAGACCTGGCTGG	242	
	30	GAGGGTGGCGGAGGG		
10	31	CCGGTGGTTCCACCCTAG	177	
12	32	GGGAGGAGCAGCGCCTT		
	33	TGCTGGCGGTCGTCTCC	210	
13	34	CGCCTGCCCAGCTTC		
14/3'UTR	35	TGGGATGATTATTTTCTGTTCTATTTGT	292	
14/3 OIR	36	GAGTAGACACTGCTTGAGGGAAAAA		
10	37	GCGTCCTGTCCACACCCA	209	
14/3'UTR	38	TGAACTGATTTATTTTTATGGCAACC		
4 - 1 - 1 - 1		GCCGATTCCGCAAGAAC	228	51o7a
14/3'UTR	39	GAGGAAGAGATGTGACTGCCAAGA		
	40	CAGTTTACACGGGTAGTGGATTGAC	340	
14/3'UTR	41	GAAGAGATGTGACTGCCAAGAGG		
	42	CCTCTTGGCAGTCACATCTCTTC	252	
14/3'UTR	43	ACAAATAGAACAGAAAATAATCATCCCA		
	44	CTAACTCAAAATGGGTCACGGAT	217	5lo1a
5'UTR/prom	45	ATTGCTTCTGCGGGTTGTGT		
	46		212	
5'UTR/prom	47	GAGAGCCGACCCGTGACC GCTGATACTGAGGATGGATTCTGG		
	48		216	51o4a
5'UTR/prom	49	TGAAAACACAACCCGCAGAAG	12.0	
	50	TGCACCTGGCAAATGGCTT	255	5lonrra,5lonrrb
5'UTR/prom	51	AAAGAACAGCGTTGGTGGAT	- 255	
	52	CAAATTCATTGTGTTGCATGTG	172	
5'UTR/prom	53	AACTTAGCCGAGATCAATACACGC	-\	
	54	GCAAATGCCTGGAAGGGTG	112	
5'UTR/prom	55	GCACAAACCCAAGACAGTATGAGG	112	
	56	CGGCGGGATGTGAAGTC	 	
5'UTR/prom	57	TGGCACTGAGAACTTGGGGA	192	
	58	ACTGGGGCAACCTCGGCT		
5'UTR/prom	1	GCTCCAGAATCCATCCTCAGTATC	154	
3 0210, P20	60	GCCTCTGCTCTCCCCAAGTTC		L